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Pred. No.

AX351053 Sequence
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AX614731 Sequence
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BD059583 Secreted G29800 human STS S BD118467 EST and e Z61642 H. Bapiens C A97176 Sequence 22 A97258 Sequence 10 BD076553 Method of BD076635 Method of AF108246 Mugil cep AY022619 Oryza sat Z57794 H. Bapiens C AF073674 Chaerophy		linear PAT 06-FEB-2002	Vertebrata; Euteleostomi; i; Hominidae; Homo.	e,м.Е., Michelotti,Б.F., , Kongpachith,А.,		Length 10; 0; Indels 0; Gaps 0;	linear PAT 23-NOV-2002	and nucleic acids coding
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C 139 1440 1441 1443 1445 1445 150		RESULT 1 AX351053 LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	ម ល	source BASE COUNT ORIGIN	Query Mate Best Local Matches Qy	RESULT 2 AX537678/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS	ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE
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ATH52101.7

Arabidopsis thaliana T-DNA flanking sequence, left border, clone 050E05.

AJ521017

AJ521017.1 GI:26789253

left border; T-DNA flanking sequence.
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red. No. 1.5e+05;
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1 (bases 1 to 39)
Wiedmer, T. and Sims, P.J.
Methods and compositions to alter the phosphatidylserine and other clot-promphospholipids
phospholipids
Location/Qualifiers
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1 (bases 1 to 36)
Van Grinsven, M. Quirinius. Joseph. Marie., De Haan, P. Theodorus.,
Gielen, J. Jacobus. Ludgerus., Peters, D. and Goldbach, R. Willem.
Constructs containing impatiens necrotic spot tospovirus RNA amethods of use thereof
methods of use thereof
Patent: US 5773700-A 19 30-JUN-1998;
Location/Qualifiers
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Impatiens necrotic spot virus
Impatiens necrotic spot virus
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tos
1 (bases 1 to 36)
Gielen, J.J. and Goldbach, R.W.
RECOMBINANT TOSPOVIRUS DNA CONSTRUCTS AND PLANTS COMPRISI
CONSTRUCTS
Patent: EP 0566525-A 19 20-OCT-1993;
SANDOZ LTD (CH); SANDOZ AG (DE)
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/organism="Impatiens necrotic spot virus"
/wol_type="genomic DNA"
/db_xref="taxon:11612"
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Sequence 19 from patent US 5773700.
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Sequence 19 from Patent EP0566525
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A78758.1 GI:6090360
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                                                                                                                                                                                                                     S Balzergue, S.

S Balzergue, S.

Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               Erunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequence of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
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Nucleic acids containing single nucleotide polymorphisms methods of use thereof
Patent: WO 0140521-A 5815 07-JUN-2001;
Curagen Corporation (US)
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'cultivar="Wassillewskija"
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1 (bases 1 to 63)

Zhang, Y., Strissel, P., Strick, R., Chen, J., Nucifora, G., Le Beau, M.M., Larson, R.A. and Rowley, J.D.

Genomic DNA breakpoints in AML1/RUNX1 and ETO cluster with topoisomerase II DNA cleavage and DNase I hypersensitive sites in
                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
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Catarrhini;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Homo sapiens isolate 1
sequence.
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WO 02053728-A 434 11-JUL-2002
Patent: WO 02053728-A 323 ... Elitra Pharmaceuticals, Inc. (US)
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               (2002)
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Mismatches 0;
                                             2 (bases 1 to 63)
Zhang,Y. and Rowley,J.D.
Direct Submission
Submitted (19-SEP-2002) Department of Me
Chicago, 5841 S. Maryland Ave., MC2115,
Location/Qualifiers
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/mol type="genomic DNA"
/isolation source="acute m/db_xref="taxon:9606"
/chromosome="21"
/map="21q22"
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/mol type="genomic DNA"
/isolation source="acute m
/db_xref="taxon:9606"
/chromosome="8"
/map="8q22"
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/map="t(21;8) (q22;q22)"
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/mol_type="genomic DNA"
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/gene="RUNX1"
/note="synonym: AML1"
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Candida albicans
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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/gene="CBFA2T1"
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Gene disruption methodologies for drug target
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Elitra Pharmaceuticals, Inc. (US)
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Gene disruption methodologies for drug target
Patent: WO 02053728-A 3787 11-JUL-2002;
Blitra Pharmaceuticals, Inc. (US)
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/mol_type="genomic DNA"
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B Balzergue, S.

Direct Submission

L Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                Gaps
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T-DNA integration into the Arabidopsis genome depends on sequ
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Arabidopsis thaliana T-DNA flanking sequence, left border
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'cultivar="Wassillewskija"
'db_xref="taxon:3702"
'clone="135F01"
'clone_lib="Arabidopsis thaliana
                                                                                                                                                                                              core 10; DB 17;
red. No. 1.4e+05;
Mismatches 0;
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/mol type="qenomic DNA"
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note="T-DNA flanking sequence"
                                             organism="Homo sapiens"
clone_lib="RPCI PAC 1,3-5"
clone="85M6"
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
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Pred. No. 1
                'db_xref="taxon:9606"
|mol_type="genomic DNA"
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Macaca mulatta
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 103)
Vartanian, J.P. and Wain-Hobson, S.
Analysis of a library of macaque nuclear mitochondrial sequences confirms macaque origin of divergent sequences from old oral polio
                                                                                                                                                                                                                                                                          Ovis aries (sheep)
Ovis aries
Ovis aries
Usaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 97)
Smith, A.J., Hulme, D.J. and Beh, K.J.
Five polymorphic ovine microsatellites
Unpublished (1994)
                                     Gaps
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isolate Cl 69 nuclear mitochochondrial gene
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PCR amplified; microsatellite; polymorphic microsatellite
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/mol_type="genomic DNA"
/db_xref="taxon:9940"
complement(12..37)
/note="binding site for PCR primer to
DB 8; I
1.3e+05;
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'standard_name="binding site for
'note="putative"
11 c 29 g 40 t
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larity 100.0%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 0;
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/standard_name="perfect G
/note="putative"
/rpt_type=other
 Score 10;
Pred. No.
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Ovis aries DNA microsatellite.
L35313
L35313.1 GI:530198
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Proc. Natl. Acad.
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Catarrhini, Cercopithecidae
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecida
Cercopithecinae; Macaca.

1 (bases 1 to 103)
Vartanian, J.P. and Wain-Hobson, S.
Analysis of a library of macaque nuclear mitochondrial s
confirms macaque origin of divergent sequences from old
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26 c 14 g 27 t
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14 g 27 t
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/mol_type="genomic DNA"
/isolate="Cl 177"
/db_xref="taxon:9544"
1. .103
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2 (bases 1 to 103)
Vartanian, J.-P. and Wain-Hobson, S.
Direct Submission
Submitted (10-APR-2002) Virology, I.
docteur Roux, Paris 75724, France
Location/Qualifiers
                                                                                               mulatta
                                                                                                   /mol_type="genomic DNA"
/isolate="Cl 69"
/db_xref="taxon:9544"
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Vartanian, J.-P. and Wain-Hobson, S. Direct Submission
Submitted (10-APR-2002) Virology, docteur Roux, Paris 75724, France Location/Qualifiers
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Macaca mulatta isolate Cl 177
sequence.
AF502361
AF502361.1 GI:21326097
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/mol_type="genomic
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RESULT

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Balzergue, S.
Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 bp DNA linear PLN 29-MAR-2003 thaliana T-DNA flanking sequence, left border, clone
PLN 29-MAR-2003 order, clone
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                                                                       AJ531685
AJ531685.1 GI:26799945
left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone 244A03.

AJ531802.

AJ531802.1 GI:26800062

AJ531802.1 GI:26800062

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                Erunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A. T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"

mol type="genomic DNA"

cultivar="Wassillewskija"

db_xref="taxon:3702"

clone="240B08"

clone_lib="Arabidopsis thaliana T-DNA insertion lines"
117 bp DNA linear PLN 29.
T-DNA flanking sequence, left border,
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EMBO Rep. 3 (12), 1152-1157 (2002)
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S Balzergue, S.

Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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AJ531828
AJ531828.1 GI:26800088
left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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T-DNA integration into the Arabidopsis genome depends on sequof pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
                        Samson, F.,
letier, G.,
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Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samsor Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="244A03"
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Balzergue, S.
Direct Submission
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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Balzergue, S.

Balzergue, S.

Balzergue, S.

Bubmitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

Gaston Cremieux, 91057 Evry cedex, FRANCE

FCR was performed on DNA from transformants of Arabidopsis thaliana

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to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and
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left border; T-DNA flanking sequence.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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T-DNA integration into the Arabidopsis genome depends on sequ
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Arabidopsis thaliana T-DNA flanking sequence, left border, 339A11.
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AJ552575.1 GI:29368722
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'clone="244G01"
'clone_lib="Arabidopsis thaliana
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'mol_type="genomic DNA"
'cultivar="Wassillewskija"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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                    /mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="339A11"
/clone lib="Arabidopsis thaliana T-DNA insertion 1. 117
/note="T-DNA flanki--
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Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified si
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Catarrhini, Hominidae, Homo
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Targeted chromosomal genomic alterations with modified strandéd oligonucleotides
Patent: WO 0173002-A 4096 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                            Length 117;
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                                                                                                                                                           Score 10; DB 8; Pred. No. 1.2e+05; D; Mismatches 0;
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Pred. No. 1.2e+05; 
; Mismatches 0;
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Mammalia; Eutheria; Primates; Catarrhin:
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http://genoplante-info.infobiogen.fr)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
a 25 c 31 g 4;
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AX266705
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Best Local Similarity
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Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Nucleic acid molecules and other molecules associated
cyst nematode resistance
Patent: WO 0151627-A 184 19-JUL-2001;
MONSANTO COMPANY (US)
Location/Qualifiers
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Novel compositions and methods for cancer
Patent: WO 03008583-A 439 30-JAN-2003;
Sagres Discovery (US)
Location/Qualifiers
                                                                                                                                                                                     Score 10; DB 6; Pred. No. 1.2e+05; Mismatches 0;
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Pred. No. 1.2e+05;
Mismatches 0;
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Patent: WO 0173002-A 4097 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers

1. .121
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
42 a 31 c 25 g 23 t
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WO0151627.
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1. .125
/organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
/note="Seq ID: 318013_ref"
/note="Seq ID: 318013_ref"
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Sequence 184 from Patent
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AX196477.1 GI:15386683
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larity 100.0%;
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Balzergue, S.

Direct Submission

Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                      129 bp DNA linear PLN 2 thaliana T-DNA flanking sequence, left border
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Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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                                                                                                     Length 128;
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hea 0;
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Pred. No. 1.2e+05;
Mismatches 0;
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mol_type="genomic DNA"
cultivar="Wassillewskija"
'db_xref="taxon:3702"
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AJ532306.1 GI:26800606
left border; T-DNA flanking sequence
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            /organism="Mus musculus"
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/db_xref="taxon:10090"
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/note="T-DNA
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    VRL 03-AUG-1993
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                                                                                                                                                           stage; Poxviridae; Chordopoxvirinae
                                                                                                                                                                                                                 DeLange, A.M. and McFadden, G. of the recombination virus, a recombinant between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
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1 (bases 1 to 133)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 26247 02-OCT-2001;
GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
JP 2001269182-A/26247
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C12N5/10,
C C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,
                    virus
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 A linear VRL 0. virus/Shope fibroma
                                                                                                                                                                                                                                                                                                                                                          virus DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                  fibroma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 14;
Pred. No. 1.2e+05;
0; Mismatches 0;
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                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Pc Leporipoxvirus.

1 (bases 1 to 131)
Upton, C., Macen, J.L., Maranchuk, R.A., De Tumorigenic poxviruses: fine analysis of junctions in malignant rabbit fibroma virus Shope fibroma virus and myxoma virus virology 166 (1), 229-239 (1988)
88322873
2842947
Original source text: Malimonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 bp DNA
human protein
RBFMVSFVA
Malignant rabbit fibroma virus Myxoma recombination site DNA.
M22117
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Malignant rabbit
/mol_type="genomic DNA"
/db_xref="taxon:10274"
22 c 27 g 45 t
                                                                                                                 Malignant rabbit fibroma virus Malignant rabbit fibroma virus
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Sequence tag and encoded
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BD050001.1 GI:22591743
JP 2001269182-A/26247.
Homo sapiens (human)
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0; Conservative (
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Hauge, B.M., Wang, M.L., Parsons, J.D. and Parnell, L.D. Nucleic acid molecules and other molecules associated cyst nematode resistance Patent: WO 0151627-A 62 19-JUL-2001; MONSANTO COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Bird, A.P.
a methylated
                                                                                                                                                                                          DB 6; L
1.2e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              loo.0%; Score 10; DB 9;
larity 100.0%; Pred. No. 1.2e+0
Conservative 0; Mismatches
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genomic Msel
                                                                                                                                                                                                  Score 10; DB Pred. No. 1.2); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             CpG island; genomic Msel fragment
Homo sapiens (human)
Homo sapiens
                                                                                                        /organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
/note="Seq ID: 240017_r
                                                                                                                                              : 240017_
12 g
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/clone_lib="CGI-1"
/dev_stage="adult"
                                                                                Location/Qualifiers
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Mammalia; Eutheria;
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HS152H1F
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N 294629
294629.
294629.
294629.
STS; single read.
Homo sapiens (human)
ISM Homo sapiens (human)
ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
NEB To (bases 1 to 135)
Deloukas, P., Buck, D., Langford, C., Ross, M.T. and Hunt, S.E.
E Direct Submission
NAL Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk
Vector: pBSIISK+
Marker stSG25547 (Primer A : TCAGCCTACACCTTGTTCCC; Primer B : GCAGCTCAAAAAGCAGATCC; amplimer size : 98 bp) was mapped to chromosome 20 using Radiation Hybrid panel Genebridge 4 (GB4).
Location/Qualifiers
1.135
.--"Homo sapiens"
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                                                                                                                                                                                                                             1-MAY-1998
OpF15C4,
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Glycine max
Slycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
                                                                                                                                                                                                                                                                                                                                   Euteleostomi
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I fragment,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="EBV lymphoblastoid cell line"
/clone_lib="SC20pF"
/dev_stage="adult"
37 c 17 g 42 t
                                                                                  Length 133;
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H. sapiens flow-sorted chromosome 20 HindIII
Bequence tagged site.
                                                                                Score 10; DB 6; I
Pred. No. 1.2e+05;
); Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
/clone="SC20pF15C4"
/sex="Female"
                                          27
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 bp
from Patent WO0151627
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Sequence 62
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HSPF15C4/c
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linear PRI 19-OCT-1995 fragment, clone 152hl,
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UK. See URL:
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Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
ce l. .139
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; E
Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                  Length 139;
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115 GAGITITGII
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E50611
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.

| (bases 1 to 142)
Parker, A. and Kornfield, I.
An improved amplification and sequencing strategy for phylogenetic studies using the mitochondrial large subunit rRNA gene
Genome 39 (4), 793-797 (1996)
96373168
                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome
                                                                                                                                         eostomi
                                                                                                                                                                                                           Genome
                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 139)
Mungall, A.J., Huckle, E., Langford, C., Ross, M.T. and Hunt, S.E.
Direct Submission
Submitted (17-APR-1997) The Sanger Centre, Wellcome Trust Genor
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk
Vector: pBSIISK+.
                                        SC6pA33A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parker, University of Maine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLU55846
Columba livia 16S ribosomal RNA gene, mitochondrial gene mitochondrial rRNA, partial sequence.
U55846
U55846.1 GI:1305540
                             STS
                                                                                                                                                                                                                                                                                                                                                                                                                     the flow-sorted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139;
                            DNA linear & 6 HindIII fragment,
                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="EBV lymphoblastoid cell line"
/clone_lib="SC6pA"
/dev_stage="adult"
/note="The estimated purity of the flow-sor'
6 library is >97%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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/organism="Columba livia"
/organelle="mitochondrion"
                                      H.sapiens flow-sorted chromosome
sequence tagged site.
294241
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens'/mol_type="genomic DNA"/db_xref="taxon:9606"/chromosome="6"
                        139 bp
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Parker, A.

Direct Submission
Submitted (19-APR-1996) Alex Partono, ME 04469-5751, USA
Location/Qualifiers
142
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               /clone="SC6pA33A6"
/sex="Female"
                                                                             Z94241.1 GI:1945235
STS; single read.
Homo sapiens (human)
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RESULT 36
HSPA33A6/c
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                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 29587 02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12N5/10,
C C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21,
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                                                                                                                                      Indel
                                                                                                                                                                                                                                                                   Sequence tag and encoded human protein.
BD053341
BD053341.1 GI:22656147
JP 2001269182-A/29587.
Homo sapiens (human)
                                                                                                        ced. No. 1.2e+05;
Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                        100.0%; Score 10; 100.0%; Pred. No.
                                            ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
JP 2001269182-A/29587
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
/mol_type="genomic DNA"
/db_xref="taxon:8932"
<1. .>142
/product="16S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 bp
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Betacellulin modification.
E50611
E50611.1 GI:18622103
JP 2000312591-A/11.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 144)
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hes 10; Conservative
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European Molecular Biology
1, 69117 Heidelberg, FRG
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Identification and characterization of differentially expressed cDNAs of the vector mosquito, Anopheles gambiae
Proc. Natl. Acad. Sci. U.S.A. 93 (23), 13066-13071 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown protein.
Anopheles gambiae
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dimopoulos, G., Richman, A., della Torre, A., Kafatos, F.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.gambiae mRNA for 3'UTR of unknown protein, clone A41
Y08165
Y08165.1 GI:1561557
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Pred. No. 1.2e+05;
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Richman, A.M.
Direct Submission
Submitted (13-AUG-1996) A.M. Richman,
Laboratory, DG Group, Meyerhofstrasse
Location/Qualifiers
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                                                                                                                                                                        from dbEST (genbank access)
Location/Qualifiers
1. .144
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="28.1 cR from top of
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28 c 35 g
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/organism="Anopheles g
/mol_type="mRNA"
/strain="G3"
/db_xref="taxon:7165"
/clone="A41"
                                                                                                                                                                                                                                                                                                     13 g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="larval"
<1. .>146
                  Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.025
Total Vol: 20 ul
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27 c
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                                                                                       Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
    Template: 10 ng
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AUTHORS
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AG3UTRA41
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      asada, R
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II IGARASHI,
REIKO SASADA, HAJIME NISHIMURA
C12N15/09, A61K38/00, A61P3/10, C07K14/47, C12P21/02//(C:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 144)
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Whitehead Institute/MIT Center for Genome Research; Physi
Mapped STSs
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    Igarashi, K.,
                                                                                                                                                                                                                                                                      /organism='Artificial Sequence'
                                                                                                                                                                                                                                                                                                                                                                                                       Length 144;
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Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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STS; STS sequence; primer; sequence tagged site
Homo sapiens (human)
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      Kobayashi, M.,
                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 6; Pred. No. 1.2e+05; D; Mismatches 0;
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                     1. .144
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
. 33 c 43 g 34 t
                                              14-NOV-2000;
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Primer B: ACTCTAAGAGGTGTGCATATAA
STS size: 144
PCR Profile:
Ito, T., Kondo, M., Tanaka, Y., Koband Nishimura, H.
Betacellulin modification
Patent: JP 2000312591-A 11 14-NOTAKEDA CHEM IND LTD
OS Artificial Sequence
PN JP 2000312591-A/11
PD 14-NOV-2000
PF 08-DEC-1999 JP 1999348531
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Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
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                                TITLE
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     AUTHORS
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2 (bases 1 to 122,)
Usmani, S. and Guan, T.S.
Direct Submission
Submitted (26-DEC-2001) Biology, Universiti Putra Malaysia, Faculty of Science and Environmental Studies, Serdang, Selangor 43400,
Malaysia
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mismatches 0;
                                                                        Location/Qualifiers
1. .149
/organism="Hemibagrus nemurus"
/mol_type="genomic DNA"
/db_xref="taxon:156983"
/clone="PCTD3"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/note="microsatellite"
/rpt_type=tandem
122. .141
/note="microsatellite"
/rpt_type=tandem
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JP 2001269182-A/32362.
Homo sapiens (human)
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II_ IGARASHI,
REIKO SASADA, HAJIME NISHIMURA
C12N15/09, A61K38/00, A61P3/10, C07K14/47, C12P21/02//(C12N15/09,
C12R1:91),
(C12P21/02, C12R1:19), C12N15/00, A61K37/02, (C12N15/00, C12R1:91)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Bagridae; Hemibagrus.

1 (bases 1 to 149)
Usmani, S. and Guan, T.S.
Identification and characterization of microsatellite
the Southeast Asian river catfish Mystus nemurus
Unpublished
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JP 2000312591-A/10.
Synthetic construct
artificial sequences.
1 (bases 1 to 147)
Ito, T., Kondo, M., Tanaka, Y., Kobayashi, M., and Nishimura, H.
Betacellulin modification
Patent: JP 2000312591-A 10 14-NOV-2000;
TAKEDA CHEM IND LTD
OS Artificial Sequence
PN JP 2000312591-A/10
PD 14-NOV-2000
PF 08-DEC-1999 JP 1999348531
Pred. No. 1.2e+05; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/db_xref="taxon:32630"
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Pred. No. 1.2e+0;
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 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                  Homo sapiens (human)
JP 2001269182-A/32362
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 153)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 14494 02-OCT-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertek Mammalia; Eutheria; Primates; Catarrhini; Homil (bases 1 to 149)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y. Sequence tag and encoded human protein Patent: JP 2001269182-A 32362 02-OCT-2001; GENSET OS Homo sapiens (human)
PN JP 2001269182-A/32362
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Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No.
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JP 2001269182-A/14494
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
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BD038248.1  
GI:22579990  
JP 2001269182-A/14494.  
Homo sapiens (human)
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Arabidopsis thaliana
Eukaryota; thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 154)
Deragon, J.-M.
SINEs from Arabidopsis thaliana
Unpublished
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Deragon, J.-M.
Direct Submission
Submitted (30-APR-2001) BIOMOVE, CNRS6547 University Blaise Pascal
24 Avenue des Landais, Aubiere 63177, France
Location/Qualifiers
1. .154
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Catarrhini; Hominidae; Homo.
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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
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/rpt_type=dispersed
a 26 c 31 g 47
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SHGC-68482 Human Homo sapiens ST
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Mammalia; Eutheria; P
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Patent: WO 0102568-A 2487 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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Sequence 2487 from Patent WO0102568.
AX072015
AX072015.1 GI:12582366
Fax: 4157259689

Email: myers@shgc.stanford.edu
Primer A: TTTGCAACTTTTCTCAATCATTTT
Primer B: TCATATCATTAAATGCAAATAGGCTT
STS size: 129
PCR Profile:
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/mol_type="genomic DNA"
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/map="6"
/clone_lib="Human"
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/organism="Homo sapiens"
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Denaturation: 9
Annealing: 6
Polymerization: 7
PCR Cycles: 3
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Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 2235 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
1. .155
/organism="Granulicatella adiacens"
/mol_type="genomic DNA"
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Velligan MD;
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Kongpachith A, S
                                                                                       Cyclin D1 -30 to -21 wild type sequence.
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RESULT 1
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cancer;

New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for regulating the expression of transgenes and for treating e.g., cancer and immunological diseases WPI; 2002-130595/17.

Sheppard LT,

DR, TW;

Latour Bruice Claim 2; Page 58; 95pp; English.

The invention describes an isolated nucleic acid regulatory sequence for a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase (Bla) promoter. Transcription regulatory sequences may be used to requlate expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin D1 can be used in cancer therapies, such as breast, colon or pancreatic cancers and familial adenomatous polyposis. Regulation of the activity of CD40L gene promoter may be used in the treatment of immunological disorders, such as autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus erythematosus (SLE), graft-ve-host disease (GVHD) and rheumatoid arthitis. Regulated expression of genes under the control of the HBV (hepatitis B)-specific core, pre-S and X promoters can be used in the hepatocellular carcinoma, and in the regulated expression of the vanH gene promoter can be used in treatment of Enterococcus infection, while regulated corpusated in treatment of Enterococcus infection, while regulated expression of the androgen receptor gene can be used in the invention corpusate cancer. This sequence represents a primer used in the invention to determine the functions of regions within the selected promoters.

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The invention describes an isolated nucleic acid regulatory sequence for a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase (Bla) promoter. Transcription regulatory sequences may be used to regulate expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin D1 can be used in cancer therapies, such as breast, colon or pancreatic cancers and familial adenomatous polyposis. Regulation of the activity of CD40L gene promoter
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LL, Kongpachith A, Sheppard LT,
                                                              ced. No. 1.4e+04; Mismatches 0;
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described in the method of the invention.
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.; 0 authorimmune diseases e.g. multiple sclerosis (MS), systematic lupus authorimmune diseases e.g. multiple sclerosis (MS), systematic lupus erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid arthritis. Regulated expression of genes under the control of the HBV (hepatitis B)-specific core, pre-S and X promoters can be used in the therapy of HBV disease, chronic hepatic insufficiency, cirrhosis, hepatocellular carcinoma, and in the regulated expression of liver cell-specific genes. Regulated expression of the vanh gene promoter can be used in treatment of Enterococcus infection, while regulated expression of the androgen receptor gene can be used in the treatment of prostate cancer. This sequence represents a mutated promoter region used in the invention to determine the regulatory regions involved in gene expression, described in the method of the invention. SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic Gaps Oligonucleotide primer SEQ ID NO 270546 for detecting SNP TSC0002178 typing, i cytosine ö 10; Indels Length of immunological disorders Set of oligonucleotides, useful for diagnosis and cell designed to detect single nucleotide polymorphisms and methylation status ·. 100.0%; Score 10; DB 24; 100.0%; Pred. No. 1.4e+04; 0 C; 3 G; 6 T; 0 other; Mismatches Berlin ő ВР 2000DE-1019173. 2001WO-IB00713 12 entry) Conservative standard; DNA; ບໍ 10 Sequence 10 BP; 1 A; Piepenbrock GAGTTTTGTT (first GAGTTTTGTT (EPIG-) EPIGENOMICS WPI; 2001-657177/75 used in the Similarity WO200177384-A2 07-APR-2000; 06-APR-2001; Homo sapiens 18-OCT-2001. 22-FEB-2002 10; 3569/c ABH70569 ABH70569; Query Match Best Local ( Olek A, Matches ABH70569 RESULT 8\$ Б õ

cancer

peptide nucleic

German.

+ Sequence Listing;

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Claim 1; SEQ ID

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This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

promoter

RESULT **ABH725** 

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detecting SNP TSC0004385

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designed to detect single nucleotide polymorphisms and cytosine methylation status
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                                                                                                                    Oligonucleotide primer SEQ ID NO 277106 for
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Coligonucleotide poly
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                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ive 0; Mismatches 0;
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                           This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. Thooligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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ABI26253 .
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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designed to detect single nucleotide polymorphisms
methylation status -
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Pred. No. 1.4e+04;
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primer;

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ABC00010-ABE82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                      mer; 88;
metabolic.
                                                                                                                                       diagnosis; PNA; cancer; CNS; cardiovascular; primer; 88;
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NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 mer; 88;
metabolic
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/tosine methylation; cardiovasc:
gastrointestinal; respiratory;
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                                                                                                                    This invention describes novel oligonucleotide primers or peptide acid (PNA) oligomers for detecting single nucleotide polymorphism and cytosine methylation status in chemically pretreated genomic oligonucleotides are used for diagnosis and/or prognosis of cancerange of diseases including immune system, gastrointestinal, respectival nervous system, cardiovascular and metabolic disorders. To oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invent NOTE: The sequence data for this patent did not form part of the specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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cytosine
                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
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                                                                                                    Sequence Listing;
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Pred. No. 1.4e+04;
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                The
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ABC00010-ABE82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABCO0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                  07-APR-2000;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
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                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABC00010-ABI82073 represent the oligomers described in the invention.
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ABI00010-ABI82073 represent the oligomers described in the invention
NOTE: The sequence data for this patent did not form part of the prin
specification, but was obtained in electronic format from WIPO at
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

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                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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1.4e+04;
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No. 1
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                                                      Homo sapiens
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                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; antisense; phospholipid scramblase I; immune disorder; cancer; inflammation; hyperproliferative; antisense therapy; phosphorothioate
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single nucleotide polymorphisms and cytosine methylation status
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                                                                                                                                              Claim 1; SEQ ID 258506; 29pp + Sequence Listing; German.
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/note= "2'methoxyethyl nucleotides"
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100.0%; Pred. No. 1.4e+04;
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                                        Piepenbrock
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Synthetic.
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                                      Olek A,
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Claim
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                                                                                                                                                                                   The invention relates to an antisense compound targetted to a nucleic acid molecule encoding phospholipid scramblase I and which specifically hybridises with and inhibits the expression of phospholipid scramblase I or which hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding phospholipid scramblase I. The invention is useful for inhibiting the expression of human phospholipid scramblase I in cells or tissues and for treating an animal having a disease or condition associated with phospholipid scramblase I, such as inflammation, an immune disorder and a hyperproliferative condition, e.g. cancer. The invention is useful for diagnostics, therapeutics and as research reagent. The present sequence is human phospholipid scramblase antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting the presence of a tumor comprises detecting the concentration of a Reg Like Protein or the presence or quantity of a nucleic acid
                                                                                                                             treating
                                                                                                                                        e.g.
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                                                                                                                  Novel antisense compounds targeted to nucleic acids encoding phospholipid scramblase I, for modulating gene expression and trainflammation, immune disorders and hyperproliferative conditions
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Pred. No. 1.4e+04;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                    0 other;
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.0; Conservative
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GAGTTTTGTT
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                    02-APR-2002;
                                      05-APR-2001;
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                                                                             Bennett CF,
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Best Local 9
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                                                                                      The invention relates to a method for detecting REG-like protein (RELP) and its nucleic acid sequence. The method is useful for detecting the presence of a tumour. Kits comprising an antibody specific for RELP and reagents for detecting the antibody, or a nucleic acid complementary to a portion of a nucleic acid encoding RELP, are useful for identifying the presence of cancer, characterise the cancer, or monitor the course of treatment of cancer. The present sequence is a PCR primer used for amplifying human RELP gene. This sequence is used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin derived protein; Ig; agonist; immunoglobulin agonist; cancer; derived protein; chromosome 1p12-13.1;
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ive 0; Mismatches 0
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                                                   26pp; English.
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globulin; cytostatic; Ig
n therapy; RELP human Ig
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PCR primers AAA59600-12 were used to amplify fragments of a gene encoding a DWF4 polypeptide. The polypeptide is a cytochrome P45 enzyme that mediates multiple steps in synthesis of brassinoster Specifically, it mediates multiple 22alpha-hydroxylation steps i brassinosteroid biosynthesis. The DWF4 polynucleotide is used fo altering the phenotype of a plant. DWF4 plants display a dramatireduction in the length of different organs, and this size reducts attributable to a defect in cell elongation. The DWF4 polynuc and polypeptides can be used in diagnostic assays and to generat antibodies, which can be used to produce immunogenic composition
                                                                                                                                                                                                                                                                                                   enzyme; brassinosteroid; 22alpha-hydroxyla elongation; PCR primer; ss.
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chromosome 1p12-13.1. The present sequence represents a PCI RELP, which is given in the exemplification of the present
                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated dwf4 polynucleotide useful for altering plants, for diagnostic assays and in the production c
                                                          10; DB 25;
No. 1.4e+04;
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100.0%; Pred. No. 1.4e+04;
ive 0; Mismatches 0;
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 AM8659019 RC3-CT034
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ALIGNMENTS	AZ851520 2M0153J18R Mouse 10kb plasmid UUGC1M l	Cione UUGCZN AZ851520 AZ851520.1		Eukaryo Mammali	<pre>1 (bases 1 to 29) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, Islam H. Longacre, S. Mahmond, M. Meenen, E. Pec</pre>	P., M., Rose, R., Stokes, R., Tingey, A., von Niederhaus 1t, D., Weiss, R.	Mouse whole genome plasmid inserts	AL Unpublished Contact: Robert B. Weiss	f Utah medica]	9095	Fax: 801 585 7177 Email: ddunn@genetics.utah.edu	Insert Length: 10000 Std Error: 0.00 Plate: 0153 row: J column: 18	Seg primer: CACACAGGAAACAGCTATGACC	High qualit	rce	/mol_type="genomic DNA" /strain="C578L/6J"	/db_xref="taxon:10090" /clone="UUGC2M0153J18"	in XL10-Gold, T1	plasmid UUGCIM library" Purified genomic DNA fro	e) was	hydrodynamically sheared b	blunt end-repaired with T	ynucleotide kinase. Adaptor oligonucleotides were ated to the blunt ends in high molar excess. The	otored DNA was purified and size-selected for 5 kb range using preparative agarose gel	or DNA was prepared from a placed from a placed from a copy-nur	ncible derivative of plasmid adaptors complementary to	The sneared, adaptored mouse DNA was vector DNA, and transformed into	and selected for ampicillin resistance."	את המים את שים	ry Match 100.0%; Score 10; DB 28; Length 29; E Local Similarity 100.0%; Pred. No. 2.2e+05;	
	RESULT 1 AZ851520 LOCUS DEFINITION	ACCESSION VERSION	SOURCE	<b>1</b> 5000	REFERENCE AUTHORS		TITLE	JOURNAL						FEATURES	ďΣ													р 6	BASE COUNT ORIGIN	Query M Best Lo	) 5
16428 QV4-HT0 1660 Q4c11f8 16597 1M0409P 11447 RPCI-11	39 RPCI-24- 7 vm99d05.x 5 vm22a04.x 7z04b06.rl	13650 Sheare 16223 Arabid 51374 Crypto	756 AV96575 12160 nae87g	217	78865 in97f0 1079 Triticu 1933 TSKH026	3248 42265 34426 BW13	36	17482 RC4-BT03 11599 PM0-NT03	120	21.2	36.7	15 6	22.	25450 BOHLD38 5029 EST00021	46	8 4	92	26192 1(3)03 17926 MuSite	17932 Musite 18018 d1-2D3	3 3	586 HUMHBC283 431 hbc2836 H	3541 z3c02a1.	35817 BX08581 36098 OSTF038	BH846 CC101	3.55	200	222	31,5	54	7677 mm27c09.r 8059 wc10a01.x	~
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
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1 (bases 1 to 31)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhau
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from
plasmid inserts
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/lab_host="E. Coli strain XL10-Gold, T1-resistan
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA fromuseulus C57BL/6J (male) was obtained from the
                                                                                                                                                    31 bp DNA linear GSS 2
10kb plasmid UUGC1M library Mus musculus
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                                                                                                                                                                                             genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Insert Length: 10000 Std Error: 0.0
Plate: 0059 row: F column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0059F05"
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Length 31;

Score 10; DB 28; Pred. No. 2.2e+05;

100.0%;

Best Local Similarity

Query Match

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Strizhov, N., Rosso, M., Li, Y. and Weisshaar, B.

Strizhov, N., Rosso, M., Li, Y. and Weisshaar, B.

Direct Submission

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion within the locus defined by clone K7M2. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German

the context of the GABI-Kat project. GABI'. Information on line

availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers
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/ organism="Arabidopsis thaliana"
/ mol_type="genomic DNA"
/ strain="Columbia 0"
/ db_xref="taxon:3702"
/ clone="GK-204F03-014508"
/ clone="GK-204F03-014508"
/ clone="lib="Arabidopsis thaliana T-DNA insertion lines"
/ note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                              Arabidopsis thaliana T-DNA flanking sequence GK-204F03-014508, genomic survey sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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Class: TDNA tagged.

Location/Qualifiers

1. .37

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines cach of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
                                                                                                                                                                                           Tracheophyta
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lines
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uj06e03.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1891132 3' similar to SW:ALBU_MERUN 035090 SERUM ALBUMIN
PRECURSOR. ;, mRNA sequence.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
servosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 37)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadz, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., St., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 653 4100 x1752
Fax: 858 6379
                                                                                                                                                                                                          ts;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is single pass sequence recovered from the left borde TDNA.
                                  bp DNA linear GSS sis thaliana TDNA insertion clone SALK_084448.42.55.x,
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Pred. No. 2.3e+05;
0; Mismatches 0;
                               BH855860
SALK 084448.42.55.x Arabidopsis tl
Arabidopsis thaliana genomic clone
survey sequence.
BH855860
BH855860.1 GI:21705450
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             larity 100.0%;
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/dev stage="adult"
/dev stage="adult"
/lab_host="DH10B"
/clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor {TGTTGGCCTACTGG}, digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano {University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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2M0096H10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0096H10 F, genomic survey sequence.
AZ822694
AZ822694.1 GI:12992602
GSS.
                                                                                                                                                                                                                                                                                                                                                                                    contact the information.
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, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished
Other ESTs: uj06e03.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USITEL: 314 286 1810
Fax: 314 286 1810
     )., Harvey, N., Schurk, R.,
Cardenas, M., McCann, R.,
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 46;
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'mol_type="mRNA"
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clone="IMAGE:1891132"
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Mus musculus
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strain="C57BL"
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a
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// Jab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
// Clone_lib="Mouse 10kb plasmid UUGCIM library"
// Note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 46)
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SALK 023483.34.55.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 023483.34.55.x, survey sequence.
BZ290066
BZ290066.1 GI:24332810
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                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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100.0%; Pred. No. 2.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                       0.00
                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0096 row: H column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 46.
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                           sex="Male"
                                                                                        Rm. 3vc,
84112, USA
Tel: 801 585 5606
Pax: 801 585 7177
plasmid inserts
Unpublished
Contact: Robert B.
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/organism="Arabidopsis thaliana"
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/strain="Columbia 0"
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
12 a 11 c 9 g 14 t
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and N.V.
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. E-mail enquiries
                                                                                                                                                                                                                               Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At4g30790
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genomic survey sequence
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Plasterk an
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

(Cypriniformes; Cyprinidae; Danio.

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (27-JAN-2003) The Sanger Institute, Wellcome T.

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail en

humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 83F10

part of the Daniokey BAC Library created by R. Plasterk

Keygene, Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.

Location/Qualifiers
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                                                                                                                                                                   92037,
                                                             Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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Pred. No. 2.3e+05;
Mismatches 0;
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/db_xref="taxon:7955"
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/tissue_type="Testis"
/note="vector pindigoBAC-536"
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Ecker, J.R.
Library of
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Location/Qualifiers
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Tracheophyta;
idicots; rosids
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1 (bases 1 to 52)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 16-FEB-2001 musculus genomic
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Cell cultures derived from root tissues"
/dev stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone_lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 ar 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
                                                                                       Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicota;
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
     cell culture Medicago truncatula
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1M0566A17R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0566A17 R, genomic survey sequence.
AZ767508
AZ767508.1 GI:12885672
GSS.
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Pred. No. 2.3e+05;
Mismatches 0
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/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF026C12EC"
                                                                                                                                                                                                                                                                                                Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 52 Std Error: 0.00
Plate: 026 row: C column: 12
                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 52 Std_Error: 0.00
Plate: 026 row: C column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
  NF026C12EC1F1098 Elicited c
clone NF026C12EC 5', mRNA 8
BF643549
BF643549.1 GI:11908770
EST.
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vj12a02.rl Barstead mouse proximal colon MPLRB6 Mus musculus cDNA clone IMAGE:921482 5', mRNA sequence.
AA529767
AA529767.1 GI:2272473
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Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact
IMAGE Consortium (info@image.llnl.gov) for further informat
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelee Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina 1 (bases 1 to 51)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dul Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M. Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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core 10; DB 29;
red. No. 2.3e+05;
Mismatches 0:
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Mismatches 0;
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BH902064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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., Shinn, P.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                      SLC,
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A Sequence-Indexed Library of Insertion Mutations in the
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                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 10; DB 28;
100.0%; Pred. No. 2.3e+05;
ive 0; Mismatches 0;
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                                                         Univer-
Rm. 308, Biomear-
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0566 row: A column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 52.
Location/Qualifiers

.**..a musculus"
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0566A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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12 GAGTTTTGTT 21
Unpublished
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 095111"
/clone="SALK 095111"
/clone="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
2 a 11 c 10 g 17 t
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Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Ga, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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SALK 091210.33.70.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 091210.33.70.x,
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core euc
; eurosids II; Brassicales, Brassicaceae, Arabidopsis,
1 (bases 1 to 60)
                                                                                          USA
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Salk Institute Genomic Analysis Laboratory (SIGN
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                       92037,
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (S
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 9203
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from t
TDNA.
Class: TDNA tagged.
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/wol_type="genomic DNA"
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2.3e+05;
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sex="male"
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lus cDNA
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Sciurognathi; Muridae; Murinae; Mus
/strain="Columbia".
/db_xref="taxon:3702"
/clone="SALK 091210.33.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used of
the site of insertion. Details of the protocols.html
                                                                                                       used ca
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0213 row: D column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 61
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Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
III, Becker,K.G. and Ko,M.S.H.
Genome*wide expression profiling of mid-gestation placent;
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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                                                                                                                                                                                           Length 60;
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CDNA Library Mus
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Pred. No. 2.3e+05;
0; Mismatches 0;
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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                      AW552498
L0213D06-3 NIA Mouse Newborn Ovary
clone L0213D06 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 61)
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                      ;
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AW552498.1
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10922068
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Lone-linker LL-Sal3 (include Sal1 sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the cDNAs were cDNAs were cloned into Sali/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan Piao."
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1 (bases 1 to 61)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                     amplified
                                                                                                                                                                                       were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Yr76a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens CDNA IMAGE:211188 5' similar to SP:A42121 A42121 HELIX-LOOP-HELIX PROTEIN ;, mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 6310
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2780
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; consortium (info@image.llnl.gov) for further informed Consortium (info@image.llnl.gov) for further informed Errace considered overall poor quality
Possible reversed clone: similarity on wrong strand Insert Length: 2780 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 61
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Pred. No. 2.3e+05;
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/db_xref="GDB:3784029"
/db_xref="taxon:9606"
/clone="IMAGE:211188"
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Seg primer: M13RP1
High quality sequence stop:
Location/Qualifiers
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                                                                               100.08;
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10; Conservative
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C
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BZ767245/c
                      BASE COUNT
ORIGIN
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AZ805922/c
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VERSION
KEYWORDS
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AUTHORS
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Matches
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                                                             2: Eco RI;
(dT) primer
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Library
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2: Eco RI;
(dr) primer
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                                                  Pharmacia)
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Parsons,J.,
Waterston
                                                                                                                         o the Pac
Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eostomi;
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen lNFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmac with a modified polylinker; Site_l: Pac I; Site_2: Eco_lst trand cDNA was primed with a Pac I - oligo(dT) prices and Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

1 a 17 c 9 g 10 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Congortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 62)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., P. Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., 7R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                     62 bp mRNA linear EST yv26e03.r1 Soares fetal liver spleen INFLS Homo sapiens IMAGE:243868 5', mRNA sequence.
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                                                                                                                                                                                                                                Length
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Pred. No. 2.3e+05;
; Mismatches 0;
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/mol_type="mRNA"
/db_xref="GDB:3793001"
/db_xref="taxon:9606"
/clone="IMAGE:243868"
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High quality
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Best Local Similarity
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EST.
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
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SOURCE
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 138564.39.05.x"
/clone="SALK 138564.39.05.x"
/clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
20 a 7 c 10 g 25 t
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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lines
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., Shinn, P.
                                                                                                                                                                                                                                                                                                                                                                                                                   genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 62)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., G., C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                             BZ767245
SALK 138564.39.05.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_138564.39.05.x, survey sequence.
BZ767245
BZ767245.1 GI:28939798
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                              Indel
                                                                                          Score 10; DB 14;
Pred. No. 2.3e+05;
Mismatches 0;
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Pred. No. 2.3e+05;
0; Mismatches 0;
Bento Soares
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DEFINITION

LOCUS

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

JOURNAL

TITLE

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1. . b,

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ImAGE:2391743"
/tissue_type="colon tumor, RER+"
/lab host="DH10B"
/clone_lib="NCI_CGAP_Co16"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Co10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 bp mRNA linear EST 02-MAY-2003 stressed bequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera CD012715. CD012715.1 GI:3032043, mRNA sequence.
                                 67 bp mRNA linear EST 18-JUN-1999 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2391743 3'TR:099523 SORTILIN PRECURSOR.;, mRNA sequence.
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Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 67)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing C Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 9; 1
100.0%; Pred. No. 2.3e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                       GI:5101282
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Homo sapiens
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wi30b12.x1 N
similar to 7
AI739301
AI739301.1
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ORGANISM
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VERSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 65)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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            0-FEB-2001
                                   genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the
2M0067N04R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0067N04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 2.3e+05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rm. 3ve,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: N column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 65.
Location/Qualifiers
65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC2M0067N04"
                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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PEATURES

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RESULT 19

Match Local

Query Ma Best Loc Matches

BASE COUNT ORIGIN

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Class: TDNA tagged
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21 GAGTTTTGTT
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AZ513784/c
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AUTHORS
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 69)
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/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotistressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: XhoI"
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t1g78510.
                                                 berries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished
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SALK 055936.38.90.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_055936.38.90.x, survey sequence.
CC178947.
CC178947.1 GI:30317498
GSS.
                                                database for abiotic stressed
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 14;
Pred. No. 2.3e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            /organism="Vitis vinifera"
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/db_xref="taxon:29760"
/clone="VVC033B04"
                                                                                                                                                                                                                         FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 033 row: B column: 04
Seq primer: T22V (V=A,C;G)
High quality sequence stop: 68.
Location/Qualifiers
         1 (bases 1 to 68)
Cushman, J.C.
An expressed sequence tag datal
Vitis vinifera var. Chardonnay
Unpublished
                                                                                                            Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014,
Tel: 775-784-1918
Fax: 775-784-1650
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0
                                                                                                                                                                                          Email: jcushman@unr.edu
PCR PRimers
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                                                                                               Contact: Cushman JC
; Vitaceae; Vitis.
1 (bases 1 to 68)
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CC178947/c
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/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 055936.38.90.x"
/clone="SALK 055936.38.90.x"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o DNA linear GSS 24-JUN-1999 clone 85M6 (70 bp), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-JUN-1999) Niederfuehr A., Physiologische Chemie I,
Theodor-Boveri-Institut fuer Biowissenschaften, am Hubland, D-97074
Wuerzburg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.3e+05;
0; Mismatches 0;
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100.0%; Pred. No. 2.3e+05
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone_lib="RPCI PAC 1,3-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Niederfuehr, A.
Thesis (1999) Universitaet Wuerzburg
2 (bases 1 to 70)
Niederfuehr, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSA247013
Homo sapiens PAC trapped exon, c. sequence.
AJ247013
AJ247013.1 GI:5262870
GSS; PAC.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              th 100.0%; Similarity 100.0%; 10; Conservative (
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Homo sapiens
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02-MAY-2003 lines

GSS

linear

genomic

155925.37.85.x,

Gadrinab Shinn,

92037, USA

(SIGNAL)

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-453b-

us-09-875

DEFINITION

LOCUS

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/clone lib="Arabidopsis thaliana TDNA insertion
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
2 a 21 c 8 g 21 t
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At1g78510
                                                                                                                                                                                                                                                                                                                                                                                                          Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., G., C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished
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max cDNA clone GENOME
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Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
Tel: 858 453 4100 x1752
                                             CC178946
SALK 055925.37.85.x Arabidopsis thaliana
Arabidopsis thaliana genomic clone SALK_0
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2.4e+05;
hes 0;
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ID: Gm-c1073-1088 5', mRNA sequence
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                                                                                                                                                                                                                                                Arabidopsis thaliana
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                                            genomic
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0360H05"
/sex="Male"
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jack
12 bp DNA linear GSS 0:
1M0360H05F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0360H05 F, genomic survey sequence.
AZ513784.1 GI:10695100
GSS.
Mus musculus (house mone.)
                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murio
1 (bases 1 to 72)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Utal.
University of Utal.
Rm. 308, Biomedical Polymers.
R4112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: H column: 05
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 72.
Location/Qualifiers
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Pred. No. 2.4e+05;
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FEATURES

EST 28-NOV-2001 SYSTEMS CLONE

Khanna

1 (bases 1 to 73) Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna , A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C

REFERENCE AUTHORS

Query Match

Matches

Best

24

RESULT

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BASE COUNT

ORIGIN

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Gaps

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Indels

72;

Length

29

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TITLE JOURNAL COMMENT

FEATURES

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TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .74

/organism="Arabidopsis thaliana"
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/clone="SALK 044140.50.70.x"
/clone lib="Arabidopsis thaliana TDNA insertion
| /note="PCR was performed on Arabidopsis thaliana lines
| each of which contains one or more TDNA insertion
| elements. The resultant fragment for each line was
| directly sequenced to determine the genomic sequence at
| the site of insertion. Details of the protocols used can
| be found at http://signal.salk.edu/tdna_protocols.html"
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76 bp mRNA linear EST 12-DEC-2000
7h42h01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3318673 3'
similar to SW:TF1B_HUMAN Q13263 TRANSCRIPTION INTERMEDIARY FACTOR
1-BETA; mRNA sequence.
BF590835
BF590835.1 GI:11683159
EST.
                                       Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 74)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 76)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 28; I
Pred. No. 2.4e+05;
                      cress)
                    (thale
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Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ecker@salk.edu
                    Arabidopsis thaliana
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BF590835/c
                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/mol_type="mRNA"
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/db_xref="taxon:3847"
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(Sudden Death Syndrome) disease"
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/clone lib="Gm-cl073"
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Xh01; The CDNA library was constructed from mRNA isolated
from 2-3 week old seedlings that were induced for symptoms
of SDS (Sudden Death Syndrome) disease by the
translocation of culture filtrate of Fusarium solani f.
sp. glycines (Plant Cell Report 18:375-380). Cultivar
Williams 82 is susceptible to the disease SDS. Plant
tissue (expanded leaves, folded leaves, and new schots)
were collected at 1, 6, 24, and 48 hrs. after incculation
and their mRNA pooled equally for cDNA construction. The
library was prepared using the Stratagene pBluescript II
SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion via methylation during first strand
synthesis. The CDNA fragments were transformed into
the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
E.coli ElectroMax DH10B host cells. Plants were inoculated
by Shuxian Li (Glen Hartman lab, University of Illinois).
Library was constructed by bears bhill and cells. Plants
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                  , Bowers
I., Schurk
                                                                      McCann
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Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., B, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., M., R., Waterston, R. and Wilson, R.

Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 21
South Memorial Parkway Huntsville, AL 35801 For further info call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by Shuxian Li (Glen Hartman lab, University of I
Library was constructed by Reena Philip and Stev
(Lila Vodkin lab, University of Illinois)."
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SALK 044140.50.70.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 044140.50.70.x, survey sequence.
BH754805
BH754805.1 GI:19035002
GSS.
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Pred. No. 2.4e+05;
Mismatches 0;
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Best Local Similarity
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Gaps

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Indels

Length 74;

Σ.

Emmert-Buck,

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DEFINITION

BH754805 LOCUS

RESULT

Б

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ACCESSION VERSION

KEYWORDS

BASE COUNT ORIGIN

Euteleostomi;

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Conservative
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BH789918/c
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ORIGIN
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VERSION
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SOURCE
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llowing HAP
subtractive
ified cDNAs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 76)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic
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                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3318673"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Co16"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) wit modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Co10 v prepared, and ss circles were made in vitro. Following purification, this DNA was used as tracer in a subtract hybridization reaction. The driver was PCR-amplified coffrom a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Сарв
found through the I.M.A.G.E. Consortium/LLNL, send email tinfo@image.llnl.gov
Trace considered overall poor quality
Seg primer: -40UP from Gibco
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ309821
1M0017C11F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0017C11 F, genomic survey sequence.
AZ309821
AZ309821.1 GI:10351196
GSS.
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100.0%; Pred. No. 2.4e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0017 row: C column: 11
Seg primer: CGTTGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
High quality sequence stop: '
Location/Qualifiers
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100
10; Conservative
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40 GAGTTTTGTT 31
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AZ309821
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unboratory Mouse DNA Resource
[http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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lines
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., Shinn, P.
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/db_xref="taxon:10090"
/clone="UUGC1M0017C11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALK 052802.43.55.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 052802.43.55.x, survey sequence.
BH789918
BH789918.1 GI:19883016
GSS.
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10; DB 28;
Pred. No. 2.4e+05;
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Arabidopsis thaliana
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Location/Qualifiers
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Arabidopsis thaliana (thale cress)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 82)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

L Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 028088.53.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines
/clone_lib="Arabidopsis thaliana TDNA insertion
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Bukaryota; thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
i (bases 1 to 82)
i (bases 1 to 82)
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
      SALK 028088.53.15.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 028088.53.15.x,
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                                                                                                                                                                                                                                                                                                                                                                               (SIGNAL)
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Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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BH790358
BH790358.1 GI:190
                                           survey sequence.
BH758559
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 82)
A Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

L DNA Res. 7, 175-180 (2000)
E 20363093
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/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/
Location/Qualifiers
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/clone_lib="Arabidopsis thaliana flower buds Col
/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
XhoI"
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mol_type="mRNA"

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'db_xref="taxon:3702"

'clone="FB065h02F"
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/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5159023"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/clone="SALK_056885.43.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html'
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                                                                                                                            Email: ecker@salk.edu
This is single pass sequence recovered from the left border
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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SALK 045875.41.40.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 045875.41.40.x,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 82;
                           Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
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2.4e+05;
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

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/mol_type="genomic DNA"
/strain="Columbia 0"
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Arabidopsis Genome
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Fax: 858
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/strain="Columbia".
/db_xref="taxon:3702"
/clone="SALK 045875.41.40.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
the site of insertion. Salk.edu/tdna_protocols.html"
o a 31 t
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1 (bases 1 to 83)

1 (bases 1 to 83)

1 (bases 1 to 83)

2 (Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished
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/dev stage="4-5 month"
/lab_host="DH10B (phage-resistant)"
/clone lib="Gong zebrafish ovary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site 1: XhoI; Site 2: EcoRI; Poly A+ RNA was isolatd from the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovary Danio rerio cDNA clone to contains Alu repetitive element;, mRNA
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260).
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Pred. No. 2.4e+05
Mismatches 0
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TDNA tagged.
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At3g59290.
Class: TDN
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AZ825100/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 84)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
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                           ion on:
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University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml) Please contact Zhiyuan Gong for further information this library (National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Singapore 119260)."
                                                                                                                                                                                                                                                                 CNS00Y3J
Arabidopsis thaliana genome survey sequence T7 end of BAC TAMU library from strain Columbia of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.
- Web : www.genoscope.cns.fr)
Location/Qualifiers
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SALK 107080.42.10.x Arabidopsis thaliana TDNA insertion ArabIdopsis thaliana genomic clone SALK_107080.42.10.x, survey sequence.
CC457158
CC457158.1 GI:31218734
GSS.
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2.4e+05;
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
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100.0%; Pred. No. 2.4
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/clone="T15113"
/clone_lib="TAMU"
/note="end: T7"
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 107080.42.10.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
is a 18 c 12 g 30 t
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AZ825100
AZ825100.1 GI:12995008
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1 (bases 1 to 85)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Ga,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                             Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
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Pred. No. 2.4e+05;
0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-184L8"
/tissue_type="Testis"
/note="Vector pindigoBAC-536"
organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                              / Bex="Male"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Clone lib="Mouse 10kb plasmid UUGCIM library"
/ Note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humphray, S.J., Huckle, E. and Durham, J.L.

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 184L8. 184L8 is part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene. Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.

Location/Qualifiers
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Danio rerio genomic clone DKEY-184L8, genomic survey sequence
BX175134
BX175134.1 GI:28006844
GSS.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Pred. No. 2.4e+05;
; Mismatches 0;
                                                             0.00
                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0100C08"
/sex="Male"
                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0100 row: C column: 08
                                                                                               Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 86.
Location/Qualifiers
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// Organism="Homo sapiens"
// organism="Homo sapiens"
// db_xref="taxon:9606"
// clone="IMAGE:4205160"
// tissue_type="adenocarcinoma (mucinous component)"
// lab host="DH10B"
// clone lib="NCI_CGAP_Co27"
// note="Organ: colon; Vector: pAMP1; mRNA made from colonic adenocarcinoma, cDNA made by oligo-dT priming.
Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library.
cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40RP from Gibco.
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nag51c01.y1 NCI_CGAP_Co27 Homo sapiens cDNA clone IMAGE:4205160 Sequence.

mRNA sequence.

BG058951.1 GI:12525948
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1 (bases 1 to 87)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished
                                                         Gaps
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100.0%; Score 10; DB 29;
100.0%; Pred. No. 2.4e+05;
tive 0; Mismatches 0;
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Pred. No. 2.4e+05;
; Mismatches 0;
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Location/Qualifiers
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Matches 10; Conser
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2M0013K21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0013K21 R, genomic survey sequence.
               Tilobi
hbc628 Human pancreatic islet Homo sapiens cDNA clone hbc628 5'end
similar to pancreatic lipase, mRNA sequence.
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ausern, A.
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., R., M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhause and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10% plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Human pancreatic islet"
/clone lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site 1: Eco RI; Site I; mRNA was prepared from normal adult human islewas directionally synthesized from the Xho I in to the EcoRI site. cDNA was size fractionated to sequences <1000 bp in size."

26 c 22 g 22 t
                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 87)
Takeda,J., Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
A molecular inventory of human pancreatic islets: sequenc
of 1000 cDNA clones
Hum. Mol. Genet. 2, 1793-1798 (1993)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
1 (bases 1 to 87)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hami
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Univ. of Chicago
5841 S. Maryland Ave., MC1028, Chicago IL 60637
Tel: 3127029116
Fax: 3127020271
Email: g-bell@uchicago.edu
Seq primer: SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
2.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hbc628"
                                                                                                                                                                                                                                                                                             Contact: Bell GI or Takeda J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone UUGC2M0013K21 R, genom
AZ778481
AZ778481.1 GI:12908169
GSS.
Mus musculus (house mouse)
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/Clone = "USCZMUUISAZI"
//BEX="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 90)
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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SALK 052462.47.95.x Arabidopsis thaliana TDNA insertion
Arabidopsis thaliana genomic clone SALK_052462.47.95.x,
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                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0013 row: K column: 21
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Class: plasmid ends
High quality sequence stop: 87.
Location/Qualifiers
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/clone="UUGC2M0013K21"
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Direct Submission
Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
University of Cambridge, Downing Street, CB2 3EH, UNITED KI
The insertion point of the P element is before base 1 of th
sequence. Further information about this P element insertic
can be found at http://www.flyseq.org.uk and
http://www.drosdel.org.uk.
Location/Qualifiers
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                                                                                                                                                                                                                          GSS 24
element
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the DrosDel second generation deficiency kit
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Drosophila melanogaster (fruit fly)

M Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pineoptera; Endopterygota; Diptera; Brachycera; Muscome Ephydroidea; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 90;
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="2R"
                                                                                                     from
                                                                                                                                                                                                                                                                                                                                                                                                                               ced. No. 2.4e+05;
Mismatches 0;
                                                                                                                                                                                  thaliana
                                                                                 Email: ecker@salk.edu
This is single pass sequence recovered
TDNA.
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Pred. No.
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/organism="Arabidopsis |
/wol_type="genomic DNA"
/strain="Columbia 0"
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Direct Sub
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Witter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="DH10B"
/clone_lib="DH10B"
/clone_lib="DH10B"
/clone_lib="DH10B"
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(individual seed fresh weight of 100-300mg). The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note that Gm-r1030 is a re-rack of Gm-c1007."
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si60h08.yl Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE IC Gm-r1030-3352 5', mRNA sequence.
AW568695
AW568695.1 GI:7233348
EST.
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Pred. No.
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Rosso, M., Striznov
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Lotus japonicus
Lotus japonicus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta, Eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
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Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Direct Submission

Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research
The First Laboratory for Plant Gene Research; 2-6-7

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)

Location/Qualifiers
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Mismatches 0;
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Mismatches 0;
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Lotus japonicus DNA, clone:LjB141g19_r,
AG227530
AG227530.1 GI:26538154
GSS.
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Lotus japonicus BAC End sequences
Published Only in Database (2002)
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Pred. No.
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AG227530/c
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AG227529
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                                                                                                                                                              Kazusa DNA Research Institute,
esearch; 2-6-7
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                    Sato, S.
Sato, S.
Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa ....
The First Laboratory for Plant Gene Research; 2-6-7
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
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A pipeline for automated high-throughput generation of F(flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and We A new Arabidopsis thaliana T-DNA mutagenised population for flanking sequence tag based reverse genetics Unpublished
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80, M., Strizhov, N., Li, Y. and Weisshaar, B
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2.4e+05;
Lag 0;
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/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                /organism="Lotus japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
/clone="LjB141g19 r"
/clone_lib="genomīc BAC libra
/note="VECTOR:pBeloBAC11"
a 9 c 22 g 22 t
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Published Only in Database (2002) 2 (bases 1 to 91) Sato S
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Pred. No. 3
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            /clone="GK-005D06-014769"
/clone="GK-005D06-014769"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through
0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 93)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., 181am, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
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1M0059J03R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC1M0059J03 R, genomic survey sequence.
AZ331545
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                                                                                                                                                                                                                                                                                                     Length 91;
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                Score 10; DB 29;
Pred. No. 2.4e+05;
0; Mismatches 0;
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: J column: 03
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 93.
Location/Qualifiers
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mol_type="genomic DNA"
strain="C57BL/6J"
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clone="UUGC1M0059J03"
xref="taxon:3702"
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TITLE

COMMENT

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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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library, 48 hours
clone L48-2261
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Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Caryophyllales; Aizoaceae; Mesembryanthemum.
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/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-2261"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR ex
, 48 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescri
EcoRI; Site_2: XhoI"

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L48-2261T3 Ice plant Lambda Uni-Zap XR expression
NaCl treatment Mesembryanthemum crystallinum cDNA
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100.0%; Pred. No. 2.4e+05;
tive 0; Mismatches 0;
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Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cushman JC
Department of Biochemistry
University of Nevada
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
i eurosids II; Brassicales; Brassicaceae; Arabidopsis.
i (bases 1 to 95)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Arabidopsis Genome
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At3946500.
Class: TDNA tagged.
                                                                                                                                                                                                                                                BH212109
SALK 007106 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_007106, genomic survey sequence.
BH212109
BH212109.1 GI:16393007
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98: TDNA tagged.

Location/Qualifiers

1. 95

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used ca
be found at http://signal.salk.edu/tdna_protocols.html"

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larity 100.0%; Pred. No. 2.4e+05;
Conservative 0; Mismatches 0;
Query Match
Best Local Similarity 100.0%; Score 10; DB 10;
Best Local Similarity 100.0%; Pred: No. 2.4e+05;
Matches 10; Conservative 0; Mismatches 0;
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AUTHORS
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